

BLAST**Basic Local Alignment Search Tool**

- Your search parameters were adjusted to search for a short input sequence.

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Protein Sequence (19 letters)Results for: ▼

residues 117-127 of SEQ ID NO: 12

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID**Description**

None

Molecule type

amino acid

Query Length

11

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Multiple alignment\]](#) NEW

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jan 5, 2010 4:42 AM
Number of letters	3,507,711,756
Number of sequences	10,280,272
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.337428	0.294
K	0.26497	0.11
H	2.091	0.61

Results Statistics

Length adjustment 1
Effective length of query 10
Effective length of database 3497431484
Effective search space 34974314840
Effective search space used 34974314840

Graphic Summary

Show Conserved Domains

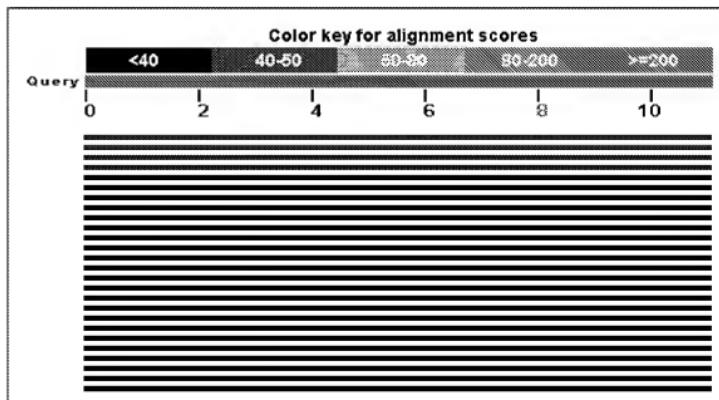
No putative conserved domains have been detected

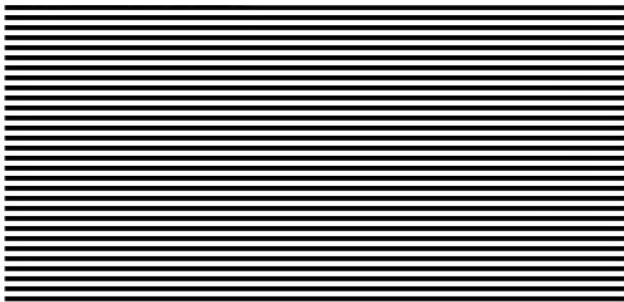


Distribution of 100 Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





The page contains a large rectangular redacted area in the upper right quadrant. This redaction is composed of approximately 20 horizontal black bars of varying lengths, creating a striped pattern that obscures sensitive information.

Descriptions

E	Score	
Sequences producing significant alignments:	(Bits)	Value
q IAAC093366.11 middle S protein [Hepatitis B virus]	41.4	0.012
q IAAC093365.11 S protein [Hepatitis B virus]	41.4	0.012
q IAAC093362.11 large S protein [Hepatitis B virus]	41.4	0.012
q IAAE36498.11 S antigen [Hepatitis B virus]	41.4	0.012
q IACT105186.11 S protein [Hepatitis B virus]	38.0	0.13
q IAAB381118.11 S protein [Hepatitis B virus]	38.0	0.13
q IBAG6745.11 hepatitis B surface antigen [Hepatitis B virus]	38.0	0.13
emb CAM58621.11 preS1 protein [Hepatitis B virus]	38.0	0.13
emb CAM58629.11 preS2 protein [Hepatitis B virus]	38.0	0.13
q IAEE54464.11 surface antigen [Hepatitis B virus]	38.0	0.13
q IAEV54241.11 S protein [Hepatitis B virus]	37.5	0.17
q IAEV54231.11 S protein [Hepatitis B virus]	37.5	0.17
q IACK69410.11 truncated middle S protein [Hepatitis B virus]	36.3	0.42
q IACK69409.11 truncated large S protein [Hepatitis B virus]	36.3	0.42
q IACK69392.11 S protein [Hepatitis B virus]	36.3	0.42
q IACK69391.11 middle S protein [Hepatitis B virus]	36.3	0.42
q IACK69390.11 large S protein [Hepatitis B virus]	36.3	0.42
q IAUQ24896.11 truncated S protein [Hepatitis B virus]	36.3	0.42
q IAUQ24893.11 truncated large S protein [Hepatitis B virus]	36.3	0.42
q IACT30881.11 large S protein [Hepatitis B virus]	36.3	0.42
q IACT79865.11 small S protein [Hepatitis B virus]	36.3	0.42
q IACT79860.11 large S protein [Hepatitis B virus]	36.3	0.42
q JISRA83889.11 hepatitis B surface antigen [Hepatitis B virus]	36.3	0.42
q JISRA83823.11 hepatitis B surface antigen [Hepatitis B virus]	36.3	0.42
q JISRA6817.11 hepatitis B surface antigen [Hepatitis B virus]	36.3	0.42
q JBMH64511.11 hepatitis B surface antigen [Hepatitis B virus]	36.3	0.42
q JACJ48743.11 S protein [Hepatitis B virus]	36.3	0.42
q JACJ48742.11 middle S protein [Hepatitis B virus]	36.3	0.42
q JACJ48741.11 large S protein [Hepatitis B virus]	36.3	0.42
q IAEV57421.11 middle S protein [Hepatitis B virus]	36.3	0.42
q IAEV57420.11 large S protein [Hepatitis B virus]	36.3	0.42
q IAEV57405.11 S protein [Hepatitis B virus] >gb ABV57406.1 ...	36.3	0.42
q IAEV57401.11 S protein [Hepatitis B virus]	36.3	0.42
q IAEV54233.11 S protein [Hepatitis B virus]	36.3	0.42
q IABV54242.11 S protein [Hepatitis B virus]	36.3	0.42
q IABV54240.11 S protein [Hepatitis B virus]	36.3	0.42
q IABV54239.11 S protein [Hepatitis B virus]	36.3	0.42
q IABV54237.11 S protein [Hepatitis B virus]	36.3	0.42
q IABV54235.11 S protein [Hepatitis B virus]	36.3	0.42
q IABV54234.11 S protein [Hepatitis B virus]	36.3	0.42
q IAEV54233.11 S protein [Hepatitis B virus]	36.3	0.42
q IABV54230.11 S protein [Hepatitis B virus] >gb ABV57420.1 ...	36.3	0.42
q IABV54228.11 S protein [Hepatitis B virus] >gb ABV54238.1 ...	36.3	0.42
q IABV54226.11 S protein [Hepatitis B virus]	36.3	0.42
q IABV54223.11 S protein [Hepatitis B virus]	36.3	0.42
q IABO37863.11 S protein [Hepatitis B virus] >gb ABQ11286.1 ...	36.3	0.42
q IABE16492.11 preS2/S protein [Hepatitis B virus]	36.3	0.42
q IAEB01501.11 S protein [Hepatitis B virus]	36.3	0.42
abj EAE00994.11 large S protein [Hepatitis B virus]	36.3	0.42
q IAAU01936.11 preS1/preS2 surface [Hepatitis B virus]	36.3	0.42
q IAAT28086.11 S protein [Hepatitis B virus]	36.3	0.42
q IAAT28085.11 middle S protein [Hepatitis B virus]	36.3	0.42
q IAAT28084.11 large S protein [Hepatitis B virus]	36.3	0.42
q IAAE15684.11 surface antigen [Hepatitis B virus]	36.3	0.42
q IBD021219.11 S protein [Hepatitis B virus]	36.3	0.42
emb CAES54049.11 S protein [Hepatitis B virus]	36.3	0.42

abg BAC9973.1	surface antigen [Hepatitis B virus]	36.3	0.42
emb CAM6536.1	pre-S2 protein [Hepatitis B virus]	36.3	0.42
emb CAM6537.1	S protein [Hepatitis B virus]	36.3	0.42
sp C67928.1 WBSCM_WENB5	RecName: Full=Large envelope protein;...	36.3	0.42
gb ADB03191.1	large S protein [Hepatitis B virus]	35.8	0.57
gb ADB02502.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02551.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02550.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02543.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02542.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb AVB2519.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb AVB2537.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02536.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02535.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02534.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02533.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02532.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02531.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02530.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02529.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02528.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02527.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02526.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02525.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02524.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02523.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02522.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02521.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02520.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02519.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02518.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02517.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02516.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02509.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02508.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02502.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb AVB2501.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02500.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02499.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02498.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02497.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02496.1	small surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02495.1	middle surface protein [Hepatitis B virus]	35.8	0.57
gb ADB02494.1	large surface protein [Hepatitis B virus]	35.8	0.57
gb ACQ82752.1	S protein [Hepatitis B virus]	35.8	0.57
gb ACQ82751.1	middle S protein [Hepatitis B virus]	35.8	0.57
gb ACQ82750.1	large S protein [Hepatitis B virus]	35.8	0.57
abg BABR7789.1	hepatitis B surface antigen [Hepatitis B virus]	35.8	0.57
abg BABR3782.1	hepatitis B surface antigen [Hepatitis B virus]	35.8	0.57

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>gb|AC005366.1| middle S protein [Hepatitis B virus]
Length=281

Score = 41.4 bits (90), Expect = 0.012
Identities = 11/11 (100%), Positives = 11/11 (100%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 214 AKYLWVWASVR 224

>gb|AC005365.1| S protein [Hepatitis B virus]
Length=226

Score = 41.4 bits (90), Expect = 0.012
Identities = 11/11 (100%), Positives = 11/11 (100%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
AKYLWVWASVR

Sbjct 159 AKYLWVWASVR 169

>gb|AC005362.1| large S protein [Hepatitis B virus]
Length=400

Score = 41.4 bits (90), Expect = 0.012
Identities = 11/11 (100%), Positives = 11/11 (100%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11

Sbjct 333 AKYLWVWASVR 343

>gb|AAF36498.1| S antigen [Hepatitis B virus]
Length=226

Score = 41.4 bits (90), Expect = 0.012
Identities = 11/11 (100%), Positives = 11/11 (100%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11

Sbjct 159 AKYLWVWASVR 169

>gb|ACI05186.1| S protein [Hepatitis B virus]
Length=226

Score = 38.0 bits (82), Expect = 0.13
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11

Sbjct 159 AKYLWXWASVR 169

>gb|ABZ81118.1| S protein [Hepatitis B virus]
Length=174

Score = 38.0 bits (82), Expect = 0.13
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11

Sbjct 153 AKYLWXWASVR 163

>dbj|BAG06746.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 38.0 bits (82), Expect = 0.13
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11

Sbjct 120 AKYLWXWASVR 130

>emb|CAM58621.1| preS1 protein [Hepatitis B virus]
Length=400

Score = 38.0 bits (82), Expect = 0.13
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11

Sbjct 333 AKYLWXWASVR 343

>emb|CAM58620.1| preS2 protein [Hepatitis B virus]
Length=281

Score = 38.0 bits (82), Expect = 0.13
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11

Sbjct 214 AKYLWXWASVR 224

>gb|ABB54464.1| surface antigen [Hepatitis B virus]
Length=195
Score = 38.0 bits (82), Expect = 0.13
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)
Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 143 AKYLWXWASVR 153

>gb|ABV54241.1| S protein [Hepatitis B virus]
Length=226
Score = 37.5 bits (81), Expect = 0.17
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)
Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 159 AKYLWAWASVR 169

>gb|ABV54231.1| S protein [Hepatitis B virus]
Length=226
Score = 37.5 bits (81), Expect = 0.17
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)
Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 159 AKYLWAWASVR 169

>gb|ACX69410.1| truncated middle S protein [Hepatitis B virus]
Length=270
Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)
Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 214 AKYLWGAWASVR 224

>gb|ACX69409.1| truncated large S protein [Hepatitis B virus]
Length=389
Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)
Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 333 AKYLWGAWASVR 343

>gb|ACX69392.1| S protein [Hepatitis B virus]
Length=226
Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)
Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 159 AKYLWGAWASVR 169

>gb|ACX69391.1| middle S protein [Hepatitis B virus]
Length=281
Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)
Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 214 AKYLWGAWASVR 224

>gb|ACX69390.1| large S protein [Hepatitis B virus]
Length=400

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 333 AKYLW WASVR 343

>gb|ACU24886.1| truncated S protein [Hepatitis B virus]
Length=215

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 159 AKYLWGWSASVR 169

>gb|ACU24883.1| truncated large S protein [Hepatitis B virus]
Length=388

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 332 AKYLWGWSASVR 342

>gb|ACT90881.1| large S protein [Hepatitis B virus]
Length=400

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 333 AKYLWGWSASVR 343

>gb|ACT79861.1| small S protein [Hepatitis B virus]
Length=226

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 159 AKYLWGWSASVR 169

>gb|ACT79860.1| large S protein [Hepatitis B virus]
Length=400

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 333 AKYLWGWSASVR 343

>dbj|BAH83888.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
AKYLW WASVR
Sbjct 120 AKYLWGWSASVR 130

>dbj|BAH83824.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 120 AKYLWGAWASVR 130

>dbj|BAH83817.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 120 AKYLWGAWASVR 130

>dbj|BAH84511.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 120 AKYLWGAWASVR 130

>gb|ACJ48743.1| S protein [Hepatitis B virus]
Length=226

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 159 AKYLWGAWASVR 169

>gb|ACJ48742.1| middle S protein [Hepatitis B virus]
Length=281

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 214 AKYLWGAWASVR 224

>gb|ACJ48741.1| large S protein [Hepatitis B virus]
Length=400

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 333 AKYLWGAWASVR 343

>gb|ABV57421.1| middle S protein [Hepatitis B virus]
Length=281

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 214 AKYLWGAWASVR 224

>gb|ABV57415.1| large S protein [Hepatitis B virus]
Length=400

Score = 36.3 bits (78), Expect = 0.42
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 0/11 (0%)

Query 1 AKYLWVWASVR 11
Sbjct 333 AKYLWGAWASVR 343